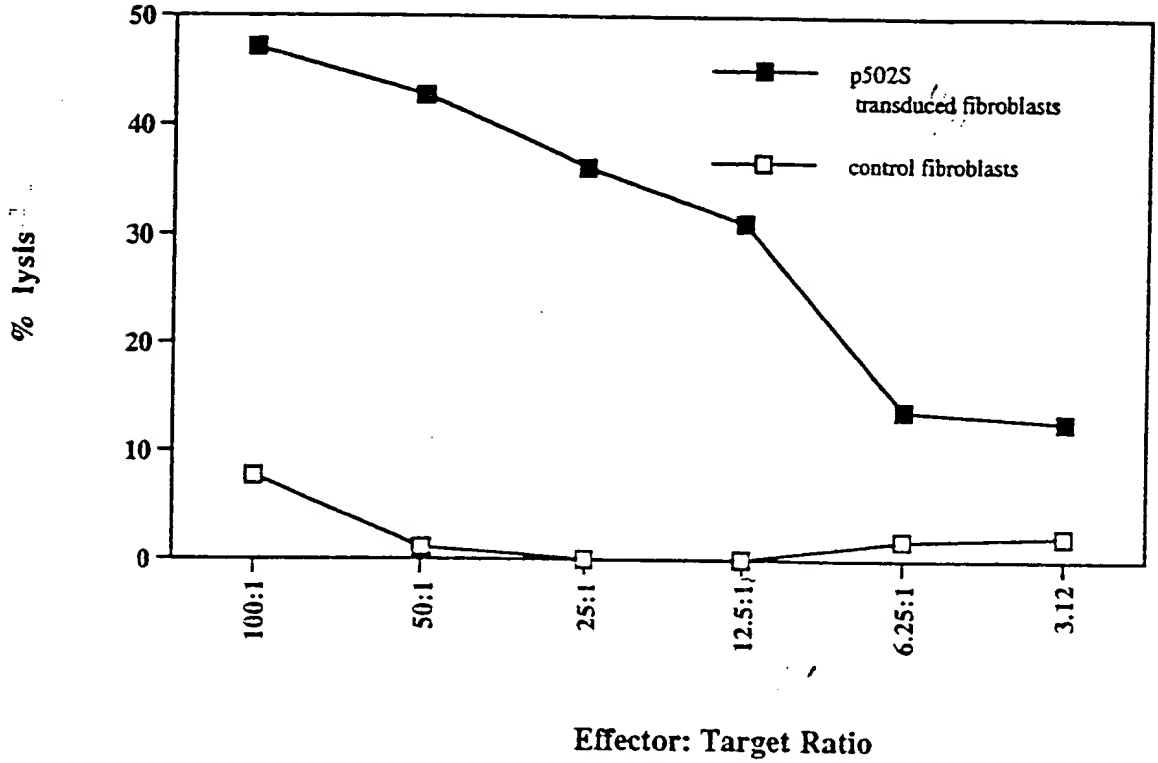

50
40
30
20
10
0
% lysis
p502S
transduced fibroblasts
control fibroblasts
100:1
50:1
25:1
12.5:1
6.25:1
3.12
Effector: Target Ratio

FIG. 1

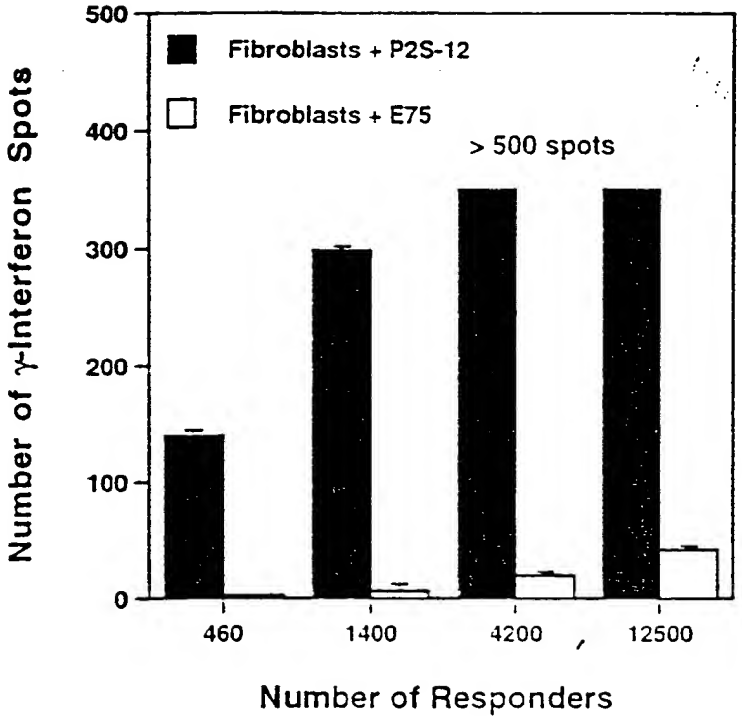

500
400
300
200
100
0
Number of γ-Interferon Spots
Fibroblasts + P2S-12
Fibroblasts + E75
> 500 spots
460
1400
4200
12500
Number of Responders

FIG. 2A

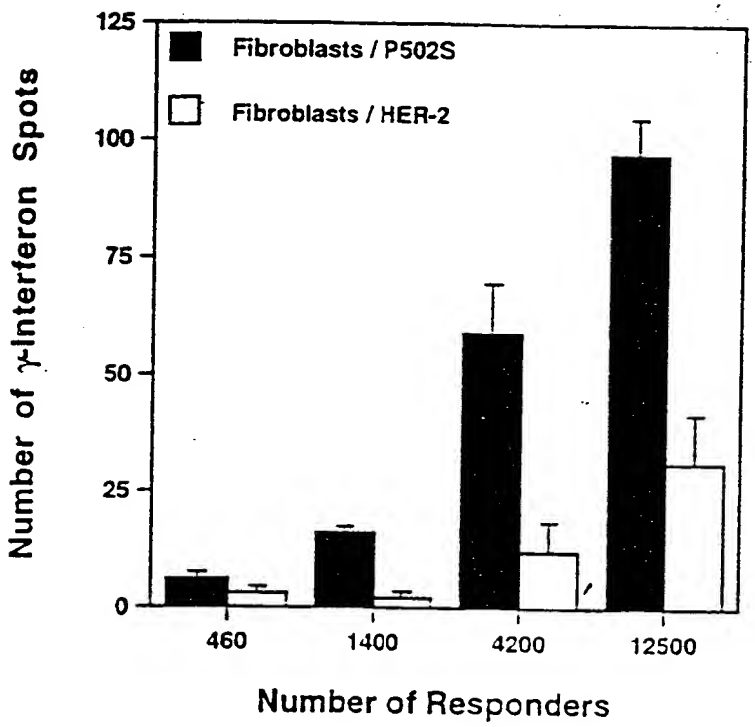

125
100
75
50
25
0
Fibroblasts / P502S
Fibroblasts / HER-2
Number of γ-Interferon Spots
460
1400
4200
12500
Number of Responders

FIG. 2B

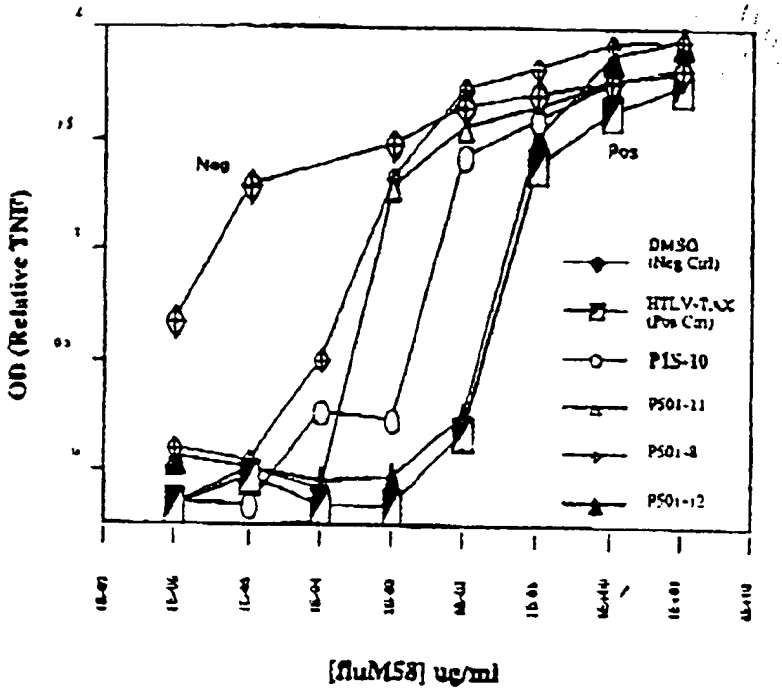

OD (Relative TNF)
Neg
Pos
DMSO
(Neg Ctrl)
HTLV-TAX
(Pos Ctrl)
P1S-10
P501-11
P501-8
P501-12
[fluMS8] ug/ml

Figure 3

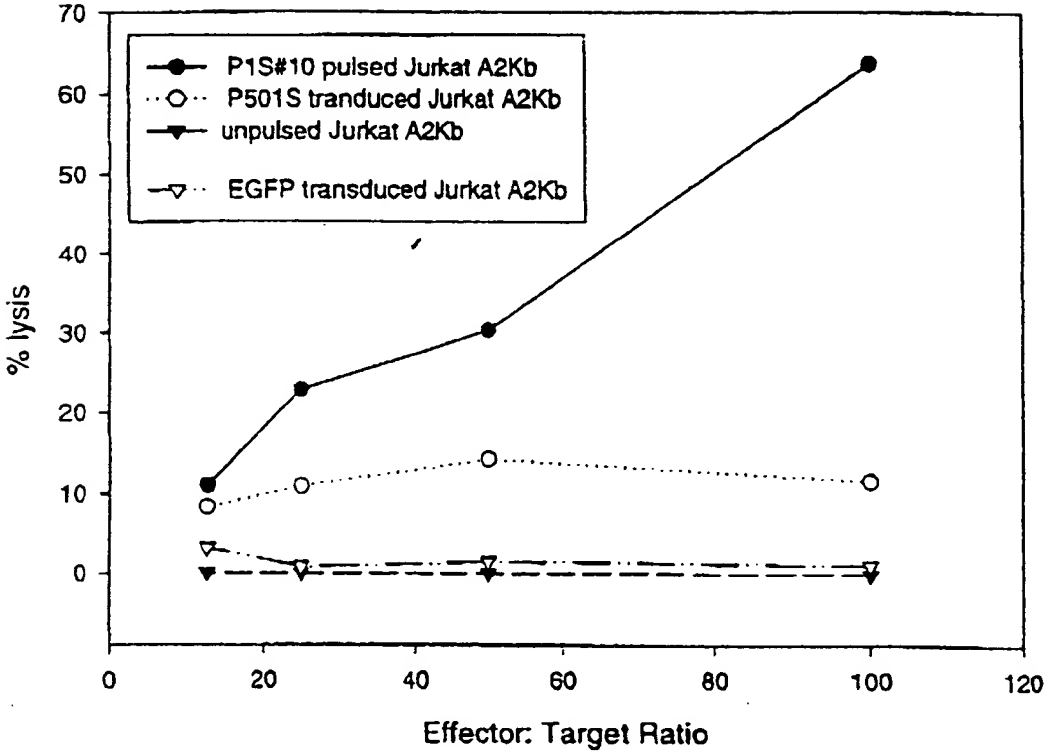

P1S#10 pulsed Jurkat A2Kb
P501S tranduced Jurkat A2Kb
unpulsed Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% lysis
Effector: Target Ratio
0
10
20
30
40
50
60
70
0
20
40
60
80
100
120

Figure 4

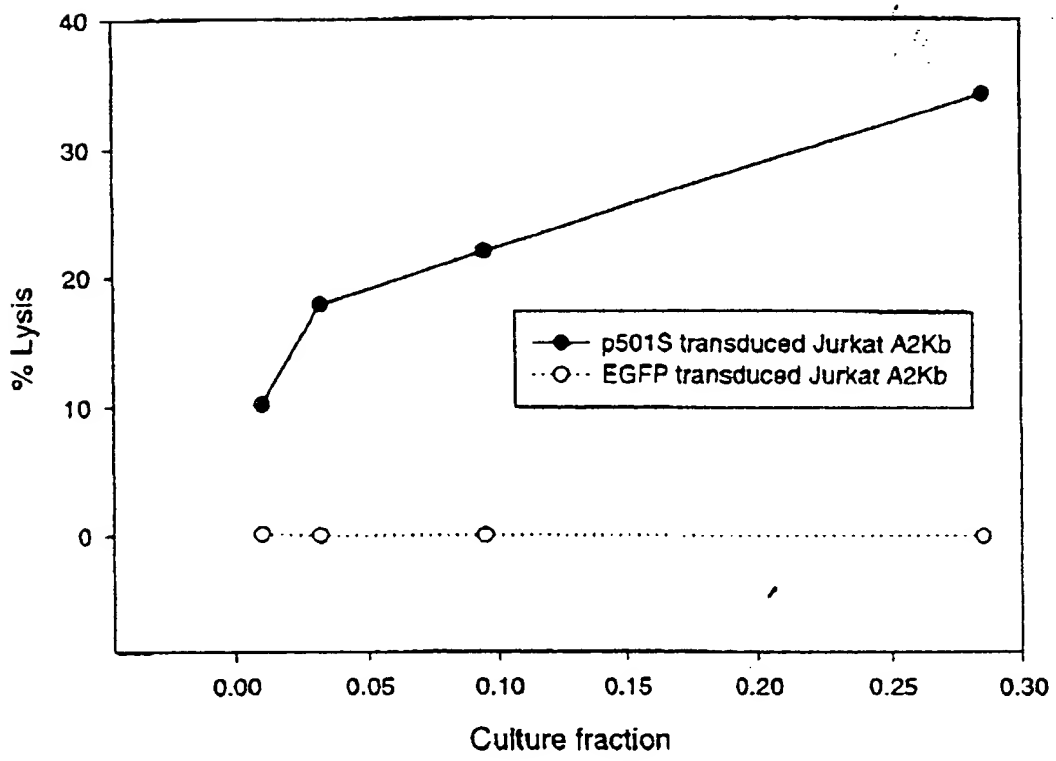

40
30
20
10
0
% Lysis
p501S transduced Jurkat A2Kb
EGFP transduced Jurkat A2Kb
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Culture fraction

Figure 5

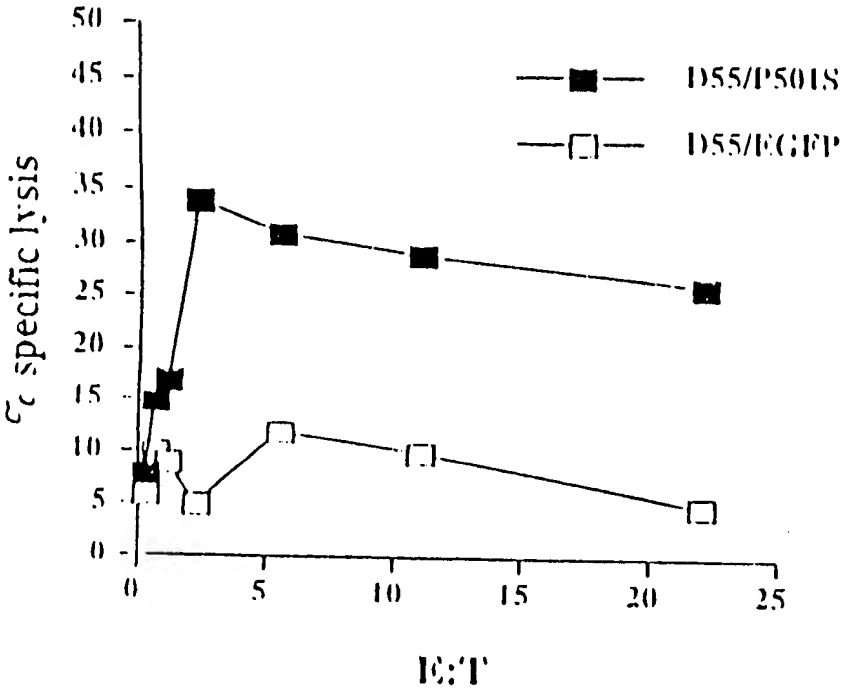

50
45
40
35
30
25
20
15
10
5
0
% specific lysis
D55/P501S
D55/ECFP
0
5
10
15
20
25
E:T

Fig. 6A

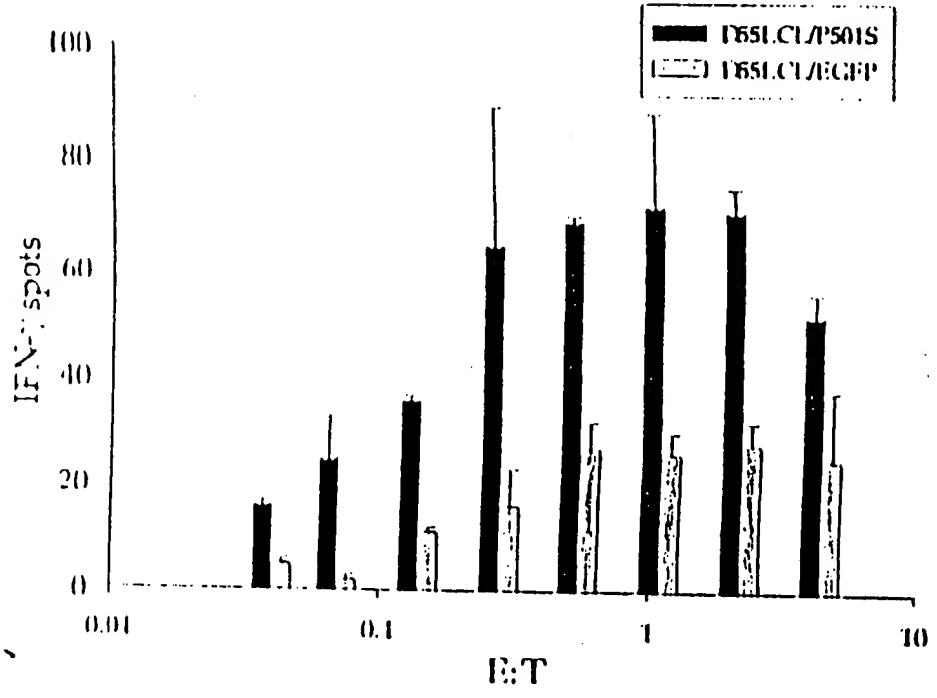
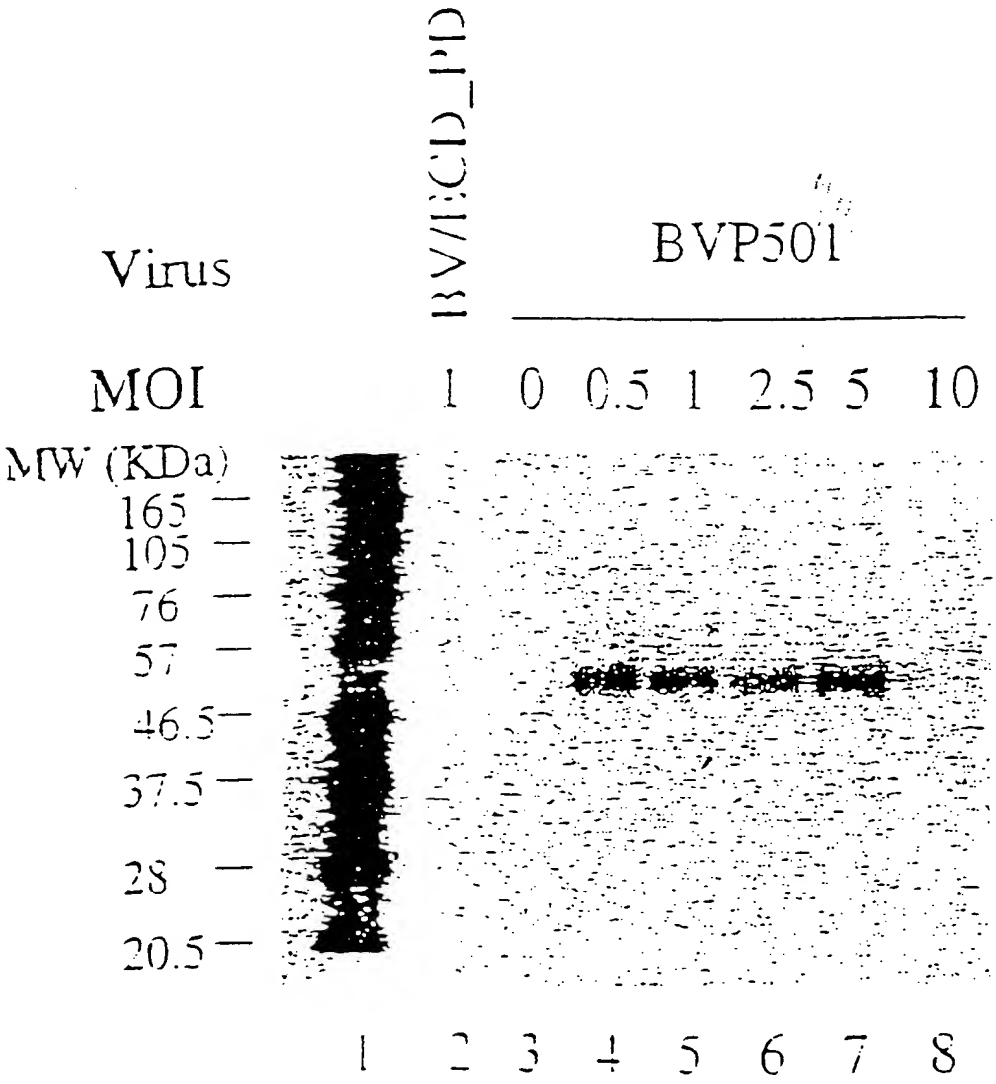

100
80
60
40
20
0
IFN-γ spots
D65LCL/P501S
D65LCL/ECFP
0.01
0.1
1
10
E:T

Fig. 6B

Expression of P501S
by the Baculovirus Expression System



0.6 million high [illegible] 6-well plate were infected with an unrelated control virus BV/ECD_PD [illegible] without virus (lane 3), or with recombinant baculovirus for P501 at different MOIs (lane 4 - 8). Cell lysates were run on SDS-PAGE under the reducing [illegible] and analyzed by Western blot with a monoclonal antibody against P501S-(6E)-(4D)-. Lane 1 is the biotinylated protein molecular weight markers.

Fig. 7

Figure 8. Mapping of the epitope recognized by 10E3-G4-D3

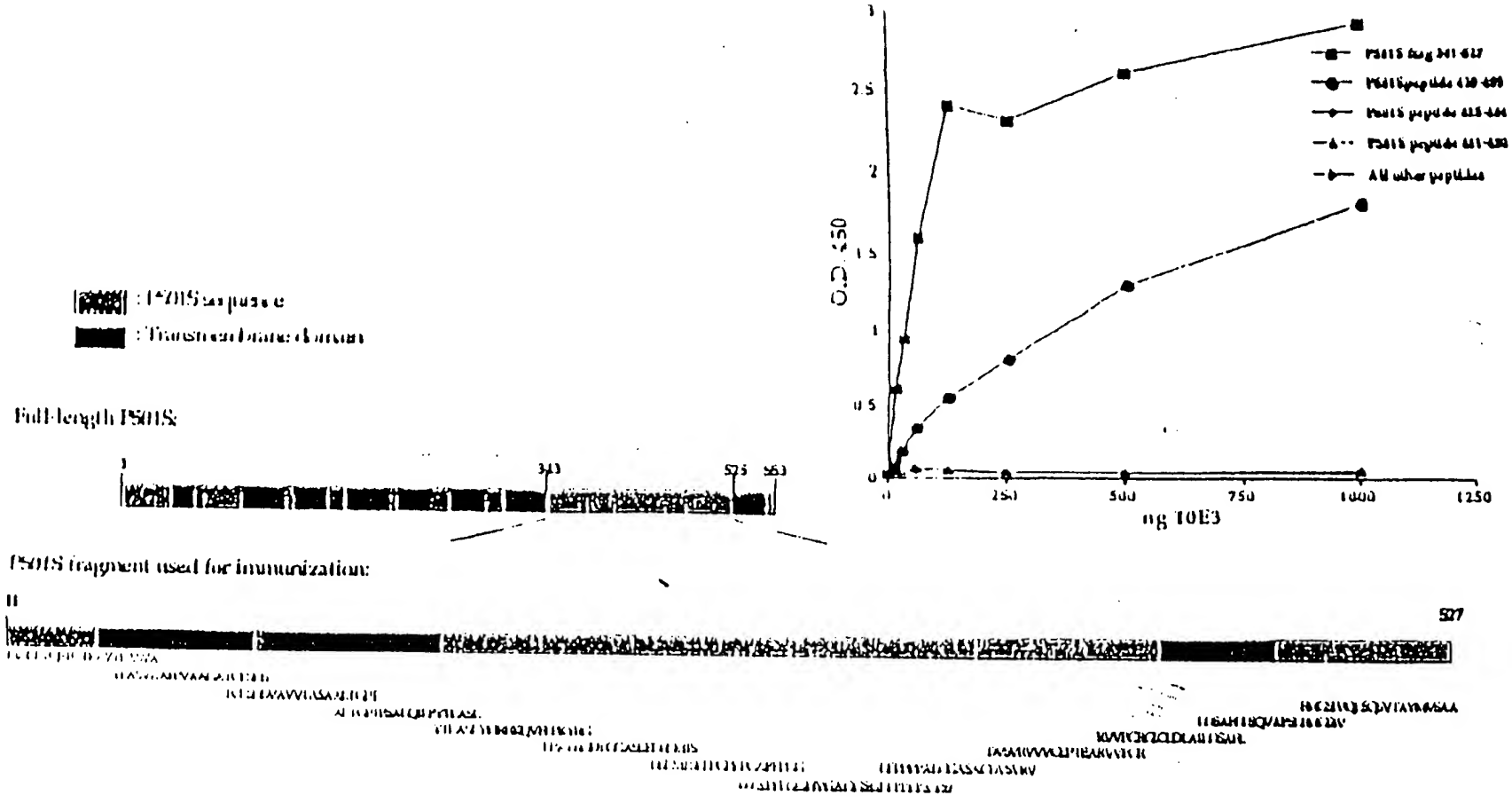


Fig. 8

Figure 1. Schematic of P501S with predicted transmembrane, cytoplasmic, and extracellular regions

MVQRLAVVSRLLRHRK AQLLLVNLLTFGLEVCLAAGIT YVPPLLLEVGVEEKFM TMVLGIGPVLGLVCVPLLGSAS

DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL AGLLCPDPRPLE LALLILGVGLLDFCGQVCFTPL

FALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAI DWDTSALAPYLGTQEE

CLPGLLTLIFLTCVAATLLV *AEEAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL*

HQLCCRMPRTLRR LPVAFLCSWMALMTFTLFYTDP VGRGLYQGVPRARPGTRARRHYDEGVR

MGSLGLFLQCAISLVFSLVM *DRLVQREGTRAVYLAS* VAAFPVAAGATCLSHSVAVVTA SAA

LTGEIFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL*

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF MGSIVQLSQS

VTAYMVSAAGLGLVALYFAT *QVVFDKSDLAKYSA*

Underlined sequence: Predicted transmembrane domain; Bold sequence: Predicted extracellular domain; *Italic sequence*: Predicted intracellular domain. Sequence in bold/underlined: used to generate polyclonal rabbit serum

Localization of domains predicted using HMMTOP (G.E. Tusnady and I. Simon (1998) Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction.J.Mol Biol. 283, 489-506.

Fig. 9

Genomic Map of (5) Corixa Candidate Genes

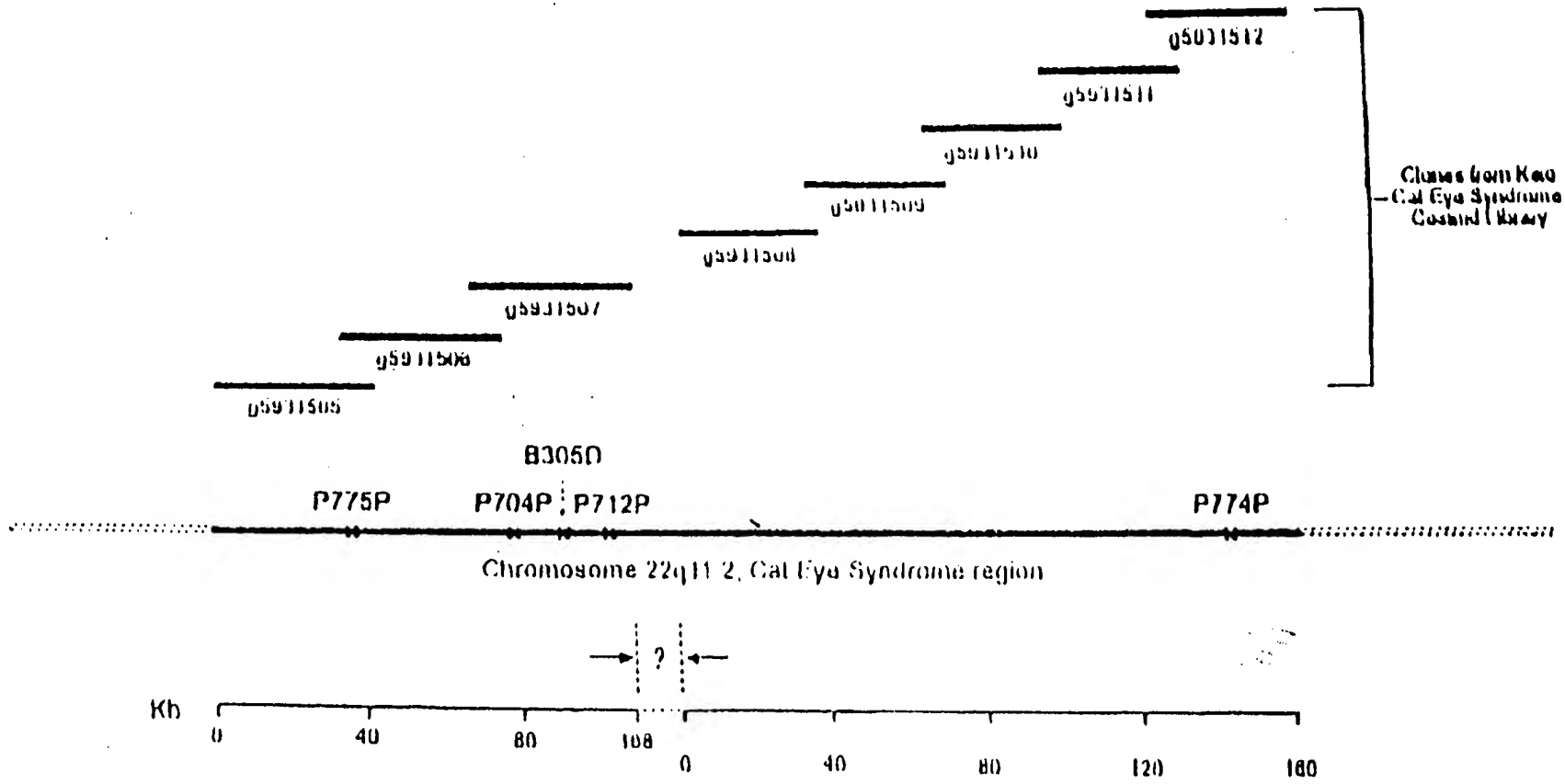


Fig. 10

FIGURE 4. Elisa assay of rabbit polyclonal antibody specificity

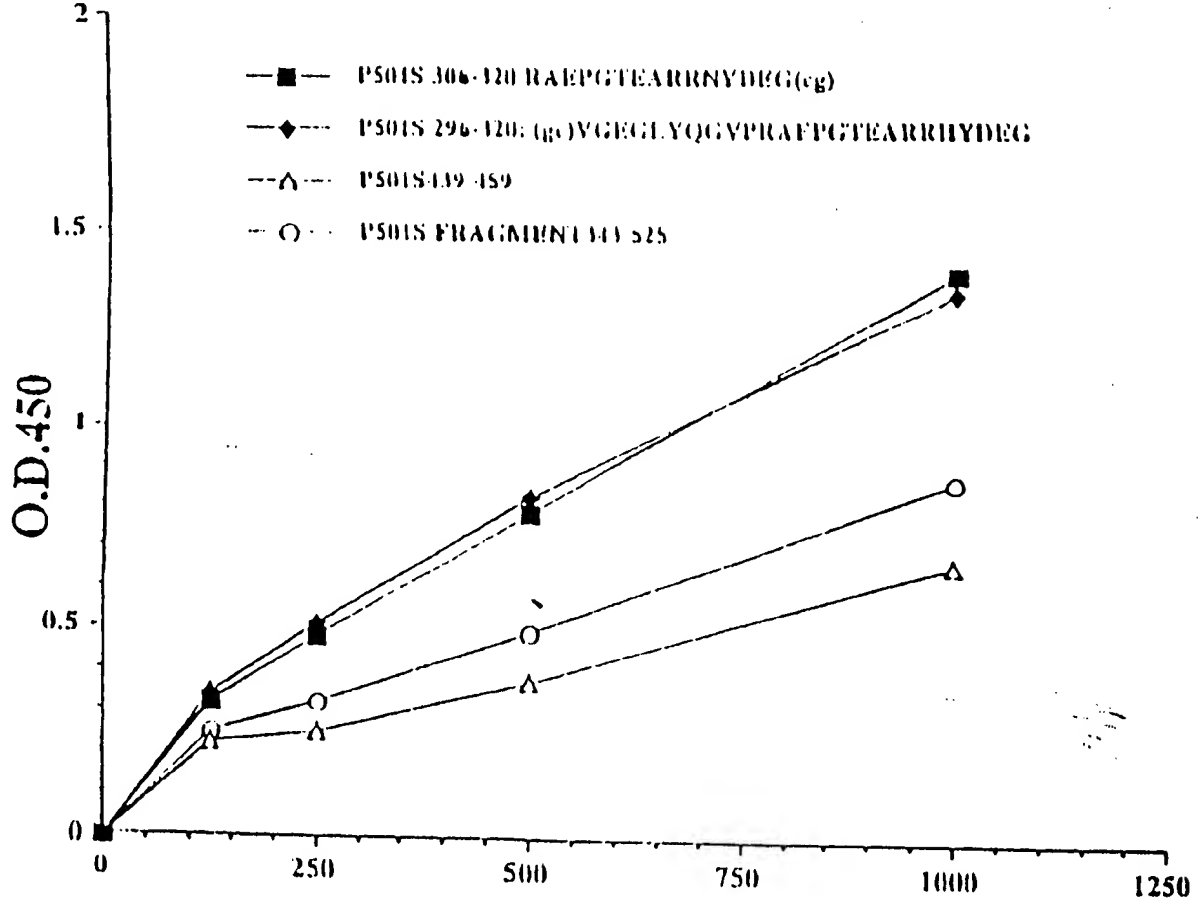
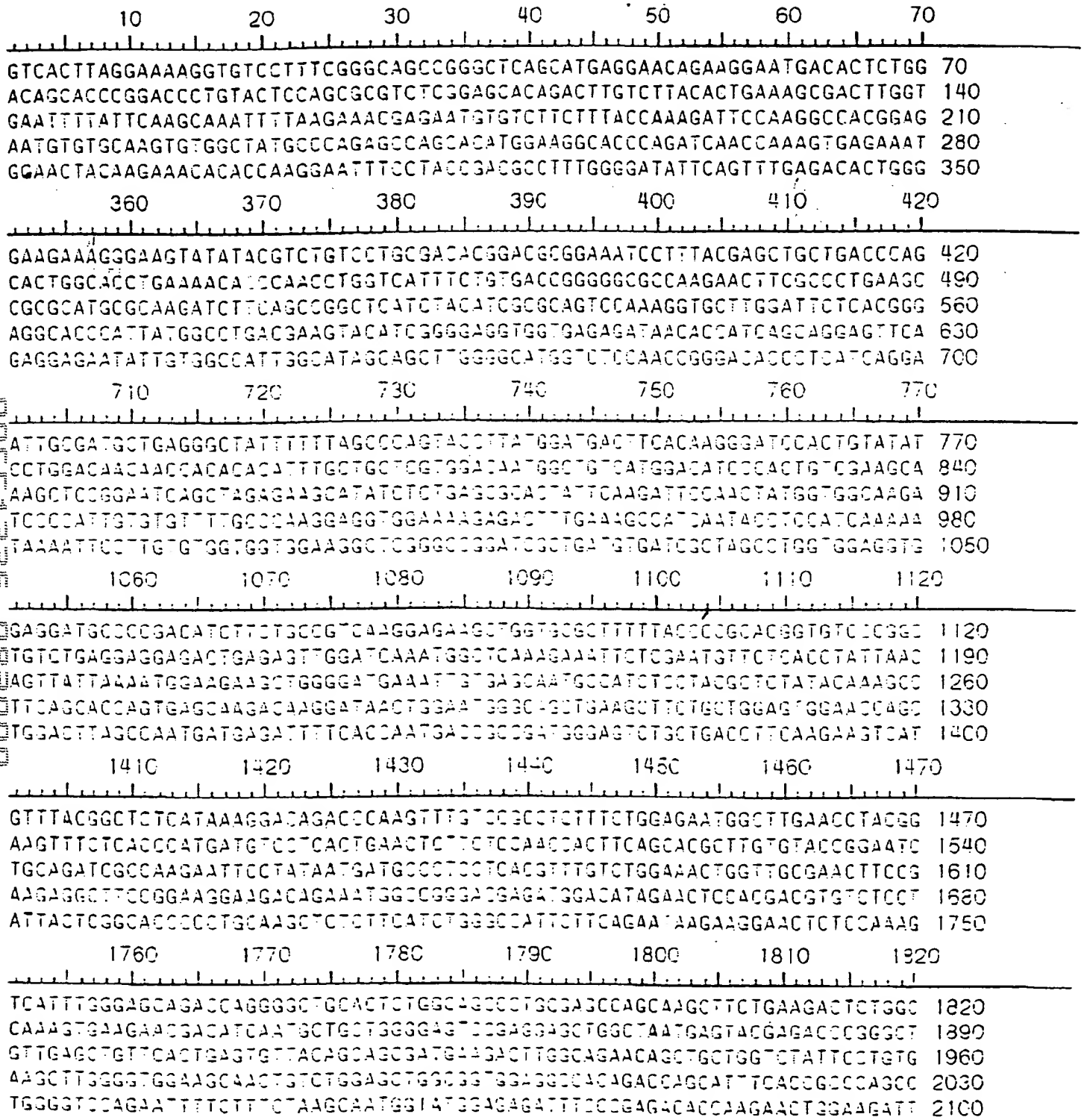


Fig. 11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GAATTTTATTCAAGCAAATTTTAAGAAACGAGAATGTGTCTTCTTTACCAAAGATTCCAAGGCCACGGAG 210
AATGTGTGCAAGTGTGGCTATGCCCAGAGCCAGCACATGGAAGGCACCCAGATCAACCAAAGTGAGAAAT 280
GGAACTACAAGAAACACACCAAGGAATTTCCTACCGACGCCTTTGGGGATATTCAGTTTGAGACACTGGG 350
360 370 380 390 400 410 420
GAAGAAAGGGAAGTATATACGTCTGTCCTGCGACACGGACGCGGAAATCCTTTACGAGCTGCTGACCCAG 420
CACTGGCACCTGAAAACATCCAACCTGGTCATTTCTGTGACCGGGGGCGCCAAGAACTTCGCCCTGAAGC 490
CGCGCATGCGCAAGATCTTCAGCCGGCTCATCTACATCGCGCAGTCCAAAGGTGCTTGGATTCTCACGGG 560
AGGCACCCATTATGGCCTGACGAAGTACATCGGGGAGGTGGTGAGAGATAACACCATCAGCAGGAGTTCA 630
GAGGAGAATATTGTGGCCATTGGCATAGCAGCTTGGGGCATGGTCTCCAACCGGGACACCCTCATCAGGA 700
710 720 730 740 750 760 770
ATTGCGATGCTGAGGGCTATTTTTTTAGCCCAGTACCTTATGGATGACTTCACAAGGGATCCACTGTATAT 770
CCTGGACAACAACCACACACATTTGCTGCTCGTGGACAATGGCTGTCATGGACATCCCACTGTCGAAGCA 840
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TAAAATTCCTTGTGTGGTGGTGGAAGGCTCGGGCCGGATCGCTGATGTGATCGCTAGCCTGGTGGAGGTG 1050
1060 1070 1080 1090 1100 1110 1120
GAGGATGCCCCGACATCTTCTGCCGTCAAGGAGAAGCTGGTGCGCTTTTTACCCGCACGGTGTCCCGGC 1120
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TTCAGCACCAGTGAGCAAGACAAGGATAACTGGAATGGGCGCTGAAGCTTCTGCTGGAGTGGAACCAGC 1330
TGGACTTAGCCAATGATGAGATTTTCACCAATGACCGCCGATGGGAGTCTGCTGACCTTCAAGAAGTCAT 1400
1410 1420 1430 1440 1450 1460 1470
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1760 1770 1780 1790 1800 1810 1820
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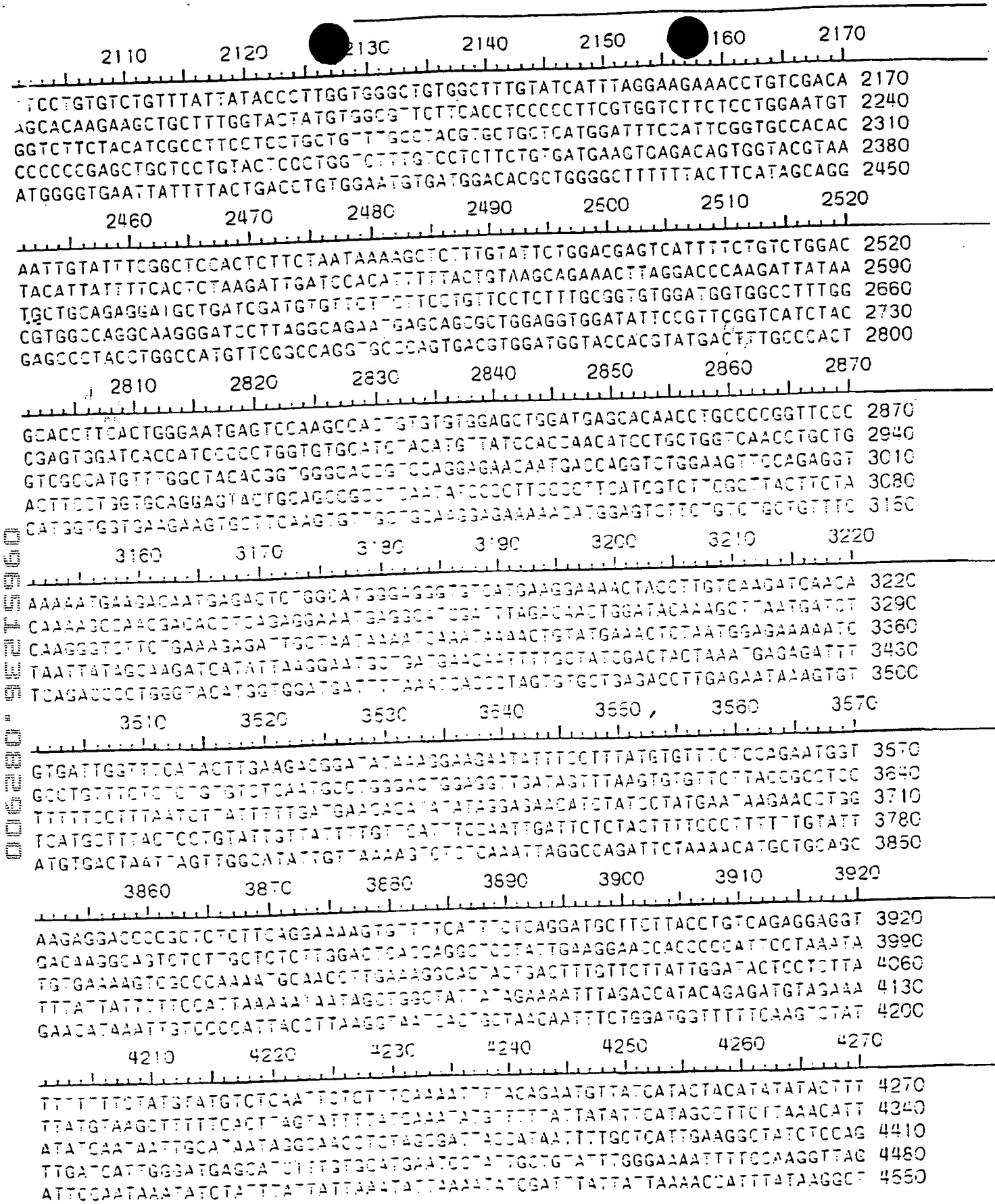
Fig. 12A (1)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GGTCTTCTACATCGCCTTCCTCCTGCTGTTGCCTACGTGCTGCTCATGGATTTCCATTCGGTGCCACAC 2310
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2460 2470 2480 2490 2500 2510 2520
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TACATTATTTTCACTCTAAGATTGATCCACATTTTTACTGTAAGCAGAAACTTAGGACCCAAGATTATAA 2590
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GAGCCCTACCTGGCCATGTTCGGCCAGGTGCCCAGTGACGTGGATGGTACCACGTATGACTTTGCCCACT 2800
2810 2820 2830 2840 2850 2860 2870
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GTCGCCATGTTTGGCTACACGGTGGGCACCGTCCAGGAGAACAATGACCAGGTCTGGAAGTTCCAGAGGT 3010
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3160 3170 3180 3190 3200 3210 3220
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CAAGGGTCTTCTGAAAGAGATTGCTAATAAAATCAAATAAAACTGTATGAAACTCTAATGGAGAAAAATC 3360
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3510 3520 3530 3540 3550 3560 3570
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3860 3870 3880 3890 3900 3910 3920
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4210 4220 4230 4240 4250 4260 4270
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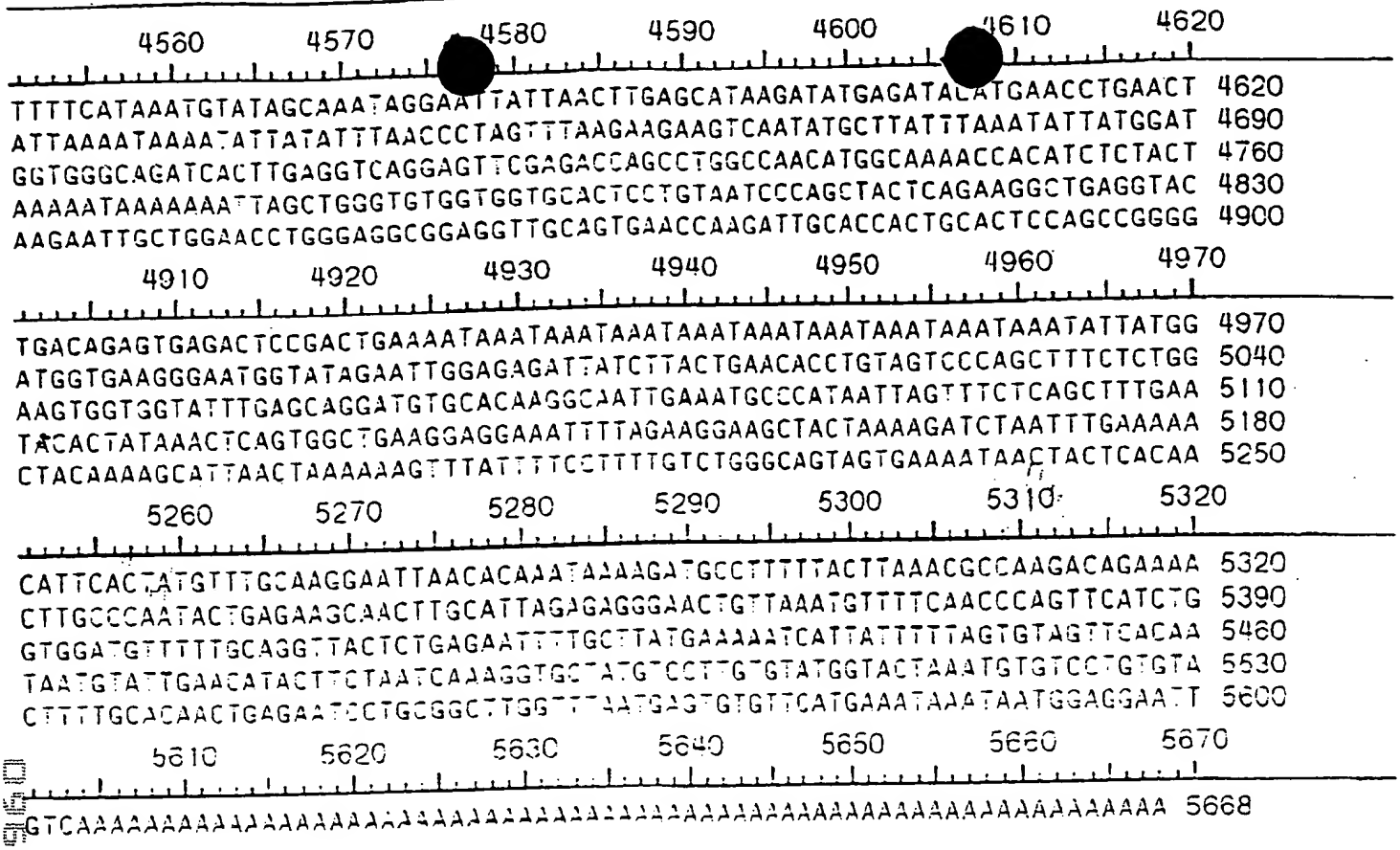
Fig. 12A(2)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4910 4920 4930 4940 4950 4960 4970
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5260 5270 5280 5290 5300 5310 5320
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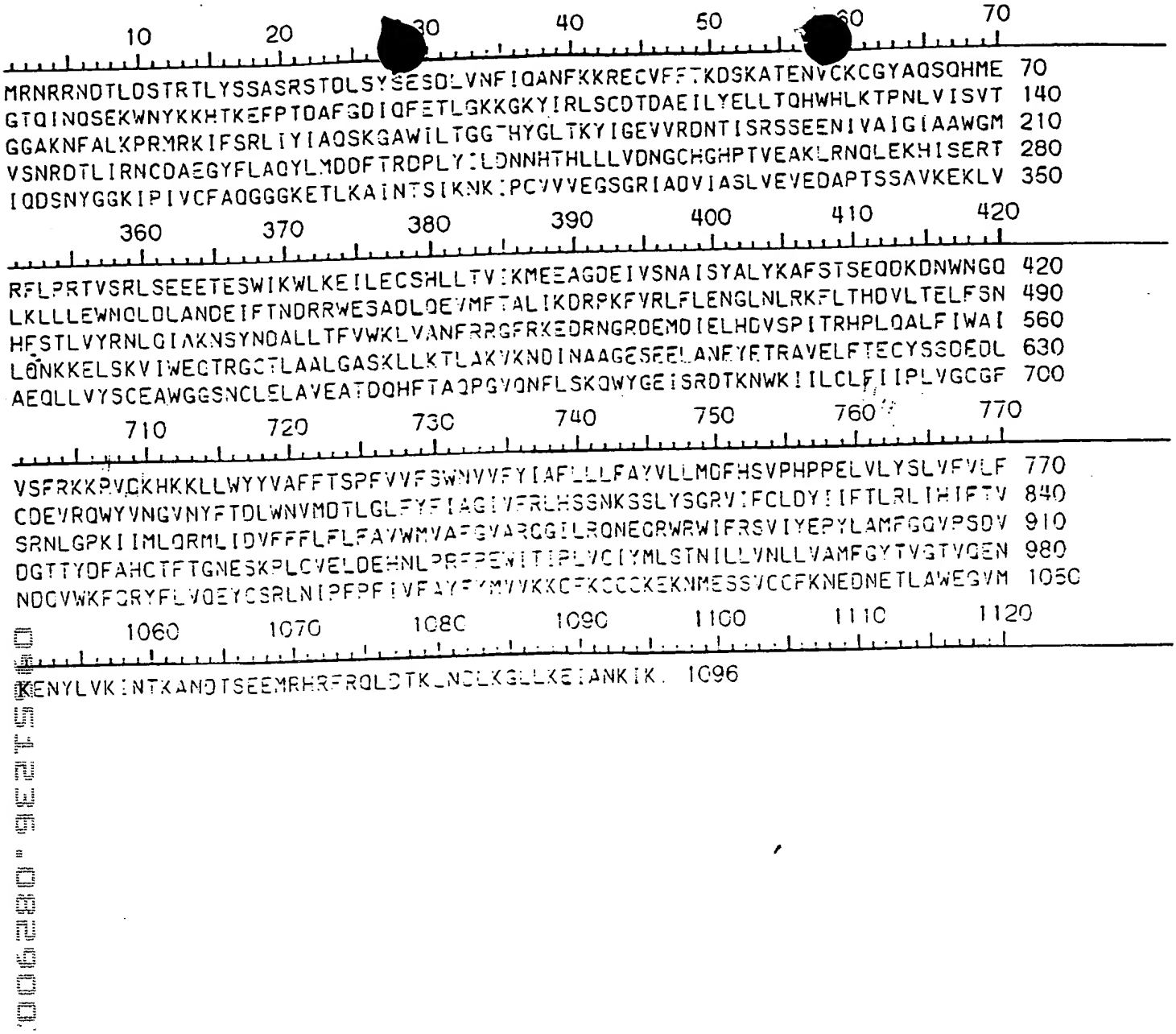
Fig. 12A(3)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GGAKNFALKPRMRKIFSRLIYIAQSKGAWILTGGTHYGLTKYIGEVVRDNTISRSSEENIVAIGIAAWGM 210
VSNRDTLIRNCDAEGYFLAQYLMDDFTRDPLYILDNNHTHLLLVDNGCHGHPTVEAKLRNQLEKHISERT 280
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360 370 380 390 400 410 420
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HFSTLVYRNLGIAKNSYNDALLTFVWKLVANFRRGFRKEDRNGRDEMDIELHDVSPITRHPLQALFIWAI 560
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1060 1070 1080 1090 1100 1110 1120
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Fig. 12B